OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 3, 2005, 21:55:55 ; Search time 693.243 Seconds
(without alignments)
11384.206 Million cell updates/sec

Title: US-09-990-249B-3
Perfect Score: 1330
Sequence: 1 ggagagagaccccaggtaca..........ctgctaaggtagagaagtgtt 1330
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Post-processing: Minimum Match 0%
Maximum Match 100%
Maximum DB seq length: 200000000
Minimum DB seq length: 0

Listing first 45 summaries

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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	183.4	13.8	106236	19	US-10-741-600-17759	Sequence 17759, A
2	135.2	10.2	6087	9	US-09-990-249A-2	Sequence 2, Appli
3	135.2	10.2	6087	18	US-10-829-491-2	Sequence 2, Appli
4	92.8	7.0	471	18	US-10-723-860-703	Sequence 703, App
5	92.8	7.0	3325	19	US-10-741-600-701	Sequence 701, App
6	92.8	7.0	3289	19	US-10-741-600-702	Sequence 702, App
7	92.8	7.0	3677	19	US-10-741-600-699	Sequence 699, App
8	92.8	7.0	3821	19	US-10-741-600-700	Sequence 700, App
9	92.8	7.0	3979	19	US-10-741-600-704	Sequence 704, App
10	92.8	7.0	4083	19	US-10-741-600-703	Sequence 703, App
11	92.8	7.0	4087	13	US-10-044-090-225	Sequence 225, App

ALIGNMENTS

RESULT 1
US-10-741-600-17759
Sequence 17759, Application US/10741600

Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17759
LENGTH: 106236
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-600-17759

Query Match 13.8%; Score 183.4; DB 19; Length 106236;
Best Local Similarity 61.7%; Pred. No. 1.1e-46;
Matches 651; Conservative 0; Mismatches 266; Indels 138; Gaps 17;

Qy 177 GGCTGAAACGCCTGTGGAAGAGGAGTCCTCTTCACCAAACGATCGGAAAACACTAATCATGG 236
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Db 5325 GGCTCAAACGCCTGCATAAGCAGGAGGACGACTCTTCAAATTATTGGAAAAACTATTAATCATGT 5384

Qy 237 TTTTCAGTTGCTTGGCT-----------------TTGATCCATACGCGTCGAGTCCACTTCATTCC 283
         | ||| |||| |||| |||||||| ||| |||||||||||||
Db 5385 TTTTCATTTGGTTTCTTCAAAACAGCCTCTTGATCCAATATCCTTTCAGTCCAACTTCATTCATTCC 5444

Qy 284 CTACCATAAGCC----AGACTTATTTGTTCAGATGGCAGCAGCCTTCCCCCTTCCTGGGTAAG-- 338
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Db 5445 CCACCTTCTAGCCAAAGAGGAGTTATTTGTTCCAGACAGCTCCCCTTCCCTTCCTTACCGTGTCCT 5504

ALIGNMENTS section column (left portion):

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13	60.2	4.5	604 18 US-10-027-632-57637	Sequence 57637, A
14	60.2	4.5	604 13 US-10-027-632-298921	Sequence 298921,
15	60.2	4.5	604 17 US-10-027-632-57637	Sequence 57637, A
16	60.2	4.5	604 17 US-10-027-632-298921	Sequence 298921,
17	60.2	4.5	607 13 US-10-027-632-5608	Sequence 5608, Ap
18	60.2	4.5	607 17 US-10-027-632-5608	Sequence 5608, Ap
19	59.8	4.5	353 18 US-10-674-124A-6831	Sequence 6831, Ap
20	59.4	4.5	760 18 US-10-363-345A-4953	Sequence 4953, Ap
21	59.4	4.5	760 10 US-10-363-345A-4954	Sequence 4954, Ap
22	59	4.5	19167 18 US-09-764-891-8028	Sequence 8028, Ap
23	58.8	4.4	233060 13 US-10-087-192-97	Sequence 97, Appl
24	58.8	4.4	634 19 US-10-643-775-1051	Sequence 1051, Ap
25	58.2	4.4	253 18 US-10-674-124A-18874	Sequence 18874, A
26	58.2	4.4	613 19 US-10-643-775-1081	Sequence 1081, Ap
27	58	4.4	122 18 US-10-674-124A-21464	Sequence 21464, A
28	58	4.4	150351 19 US-10-322-281-453	Sequence 453, App
29	57.6	4.4	1196 17 US-10-369-493-28676	Sequence 28676, A
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31	57.4	4.3	65253 17 US-10-085-117-331	Sequence 331, App
32	57.4	4.3	90650 14 US-10-322-696-37	Sequence 37, Appl
33	57.4	4.3	111206 13 US-10-087-192-1957	Sequence 1957, Ap
34	57.2	4.3	403 18 US-10-674-124A-2452	Sequence 2452, Ap
35	57.2	4.3	446 18 US-10-674-124A-3825	Sequence 3825, Ap
36	57.2	4.3	165554 13 US-10-087-192-1633	Sequence 1633, Ap
37	57.2	4.3	52764 13 US-10-087-192-391	Sequence 391, Ap
38	57	4.3	84826 13 US-10-087-192-127	Sequence 127, App
39	57	4.3	285 18 US-10-674-124A-26049	Sequence 26049, A
40	56.8	4.3	434 19 US-10-643-775-740	Sequence 740, App
41	56.8	4.3	609 19 US-10-723-860-631	Sequence 631, App
42	56.8	4.3	101270 18 US-10-723-860-631	Sequence 631, App
43	56.6	4.3	216 18 US-10-674-124A-26426	Sequence 26426, A
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: March 3, 2005, 12:39:24 ; Search time 210.34 Seconds
(without alignments)
10346.346 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	DB ID	Description
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	3	59	4.4	154626	4	US-09-949-016-14000	Sequence 14000, A
	4	58.6	4.4	601	4	US-09-949-016-77453	Sequence 77453, A
	5	58	4.4	137226	4	US-09-949-016-13763	Sequence 13763, A
	6	57.4	4.3	49301	4	US-09-949-016-16296	Sequence 16296, A
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c	9	56.8	4.3	601	4	US-09-949-016-161244	Sequence 161244,
c	10	56.8	4.3	601	4	US-09-949-016-161245	Sequence 161245,
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c	24	56	4.2	44492	4	US-09-949-016-12953	Sequence 12953, A
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c	26	56	4.2	66933	4	US-09-544-398B-11	Sequence 11, Appl
c	27	56	4.2	66933	4	US-09-543-771B-11	Sequence 11, Appl
c	28	56	4.2	129778	4	US-09-949-016-12191	Sequence 12191, A
c	29	56	4.2	129778	4	US-09-949-016-17075	Sequence 17075, A
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c	31	55.8	4.2	601	4	US-09-949-016-158359	Sequence 158359,
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c	34	55.8	4.2	2967	3	US-08-637-823B-26	Sequence 26, Appl
c	35	55.8	4.2	2967	3	US-09-614-957D-26	Sequence 26, Appl
c	36	55.8	4.2	3757	2	US-09-016-366A-13	Sequence 13, Appl
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c	38	55.8	4.2	28366	4	US-09-949-016-16763	Sequence 16763, A
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c	45	54.8	4.1	3383	5	PCT-US95-09098-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
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; Sequence 77451, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77451
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-77451

Query Match 4.4%; Score 59; DB 4; Length 601;
Best Local Similarity 81.9%;
Matches 68; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Pred. No. 1.6e-07;

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Qy   143 CACGCTCGTCCGCTCGCTCACTCA 165
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; Sequence 77452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 3, 2005, 21:55:55 ; Search time 3172.76 Seconds
                                            (without alignments)
                                            11384.206 Million cell updates/sec

Title: US-09-990-249B-2
Perfect score: 6087
Sequence: 1 cccgggaggtcccttcatc.........ctgtaactgagctaacataa 6087

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 296923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_NA:*
    1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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    4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
    5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
    6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
    7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
    8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	ID	Description
1	6087	100.0	6087	9	US-09-990-249A-2	Sequence 2, Appli
2	6087	100.0	6087	18	US-10-829-491-2	Sequence 2, Appli
3	3096	50.9	5849	18	US-10-677-777-1	Sequence 1, Appli
4	2637.4	43.3	5960	10	US-09-798-883B-14	Sequence 14, Appli
5	2637.4	43.3	5960	10	US-09-326-885-14	Sequence 14, Appli
6	2634.8	43.3	18116	18	US-10-790-455-7	Sequence 7, Appli
7	2634.8	43.3	18116	18	US-10-811-136B-7	Sequence 7, Appli
8	2634.8	43.3	18116	19	US-10-940-315-7	Sequence 7, Appli
9	2633.4	43.3	3327	18	US-10-796-486-56	Sequence 56, Appl
10	2633.4	43.3	3369	18	US-10-796-486-48	Sequence 48, Appl
11	2633.4	43.3	3954	18	US-10-796-486-53	Sequence 53, Appl
12	2633.4	43.3	3954	18	US-10-796-486-57	Sequence 57, Appl
13	2633.4	43.3	3976	18	US-10-796-486-49	Sequence 49, Appl
14	2633.4	43.3	5163	18	US-10-796-486-54	Sequence 54, Appl
15	2632.8	43.3	5283	18	US-10-796-486-58	Sequence 58, Appl
16	2633.4	43.3	5325	18	US-10-796-486-50	Sequence 50, Appl
17	2632.8	43.3	5041	18	US-10-790-455-6	Sequence 6, Appli
18	2632.8	43.3	5041	18	US-10-811-136B-6	Sequence 6, Appli
19	2632.8	43.3	5041	19	US-10-940-315-6	Sequence 6, Appli
20	2632.8	43.3	5043	18	US-10-790-455-5	Sequence 5, Appli
21	2632.8	43.3	5043	18	US-10-811-136B-5	Sequence 5, Appli
22	2632.8	43.3	5043	19	US-10-940-315-5	Sequence 5, Appli
23	2632.8	43.3	5101	18	US-10-790-455-4	Sequence 4, Appli
24	2632.8	43.3	5101	18	US-10-811-136B-4	Sequence 4, Appli
25	2632.8	43.3	5101	19	US-10-940-315-4	Sequence 4, Appli
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27	2632.8	43.3	5924	18	US-10-811-136B-3	Sequence 3, Appli
28	2632.8	43.3	5924	19	US-10-940-315-3	Sequence 3, Appli
29	2632.8	43.3	5982	18	US-10-790-455-2	Sequence 2, Appli
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33	2630.2	43.2	4987	16	US-10-097-554A-3	Sequence 3, Appli
34	2630.2	43.2	4987	17	US-10-097-034A-44	Sequence 44, Appli
35	2630.2	43.2	5115	16	US-10-237-146-8	Sequence 8, Appli
36	2625.4	43.1	5376	18	US-10-492-396-7	Sequence 7, Appli
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38	2465	40.5	5613	16	US-10-128-587A-42	Sequence 42, Appli
39	2465	40.5	5613	17	US-10-128-578B-42	Sequence 42, Appli
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41	2460	40.4	4438	9	US-09-968-355-21	Sequence 21, Appli
42	2460	40.4	4516	9	US-09-968-355-24	Sequence 24, Appli
43	2460	40.4	4594	9	US-09-968-355-15	Sequence 15, Appli
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ALIGNMENTS

RESULT 1
US-09-990-249A-2

; Sequence 2, Application US/0990249A
; Patent No. US2002010411A1
; GENERAL INFORMATION:
; APPLICANT: Chiu, Ing-Ming
; TITLE OF INVENTION: Transgenic animals for screening therapeutic agents for brain t
; FILE REFERENCE: 28489/04000
; CURRENT APPLICATION NUMBER: US/09/990,249A
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER: 2001-11-21
; PRIOR FILING DATE: US 60/252745
; NUMBER OF SEQ ID NOS: 2000-11-22
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 2
; LENGTH: 6087
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotides 1-594, human FGF1B promoter; 595-3233, SV40; 3234-6(
; OTHER INFORMATION: PGL2-Basic plasmid vector (Promega)
US-09-990-249A-2

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Best Local Similarity   100.0%;
Matches 6087; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   61 ACCTGCTGTTTCCCTGGCCAACTCAGGCCTCAAAATAAACAGGATTCTGCTCAGACGGGCC 120

OM nucleic - nucleic search, using sw model

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Run on: March 3, 2005, 12:39:24 ; Search time 962.66 Seconds
(without alignments)
10346.346 Million cell updates/sec

Title: US-09-990-249B-2
Perfect score: 6087
Sequence: 1 cccgggaggtcccttcatc..........ctgtaactgagctaacataa 6087

Scoring table: IDENTITY_NUC
GapOp 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	3096	50.9	5789	3	US-08-862-431-32	Sequence 32, Appl
2	3096	50.9	5791	3	US-08-862-431-31	Sequence 31, Appl
3	3096	50.9	5793	3	US-08-862-431-29	Sequence 29, Appl
4	3096	50.9	5793	3	US-08-862-431-30	Sequence 30, Appl
5	3096	50.9	5818	2	US-08-536-559A-3	Sequence 3, Appli
6	3096	50.9	5819	2	US-08-536-559A-2	Sequence 2, Appli
7	3096	50.9	5819	2	US-08-862-431-27	Sequence 27, Appl
8	3096	50.9	5819	2	US-08-862-431-28	Sequence 28, Appl
9	3096	50.9	5938	2	US-08-536-559A-4	Sequence 4, Appli
10	3096	50.9	6092	3	US-08-536-559A-1	Sequence 1, Appli
11	3096	50.9	6092	3	US-08-862-431-26	Sequence 26, Appl
12	3091.2	50.8	12143	3	US-09-423-744A-1	Sequence 1, Appl
13	2851.2	46.8	10504	3	US-09-423-744A-19	Sequence 19, Appl
14	2647	43.5	5183	2	US-09-039-555B-18	Sequence 18, Appl
15	2645.4	43.5	5243	2	US-08-414-335-2	Sequence 2, Appli
16	2645.4	43.5	3327	4	US-09-628-730-56	Sequence 56, Appli
17	2633.4	43.3	3369	4	US-09-628-730-48	Sequence 48, Appli
18	2633.4	43.3	3954	4	US-09-628-730-53	Sequence 53, Appl
19	2633.4	43.3	3954	4	US-09-628-730-57	Sequence 57, Appl
20	2633.4	43.3	3976	4	US-09-628-730-49	Sequence 49, Appl
21	2633.4	43.3	5163	4	US-09-628-730-54	Sequence 54, Appl
22	2633.4	43.3	5283	4	US-09-628-730-58	Sequence 58, Appl
23	2633.4	43.3	5325	4	US-09-628-730-50	Sequence 50, Appl
24	2468	40.5	2479	3	US-09-050-863-4	Sequence 4, Appl
25	2468	40.5	2479	3	US-09-359-081-4	Sequence 4, Appl
26	2459	40.4	3656	1	US-08-232-463-8	Sequence 8, Appli
27	2459	40.4	3688	1	US-08-232-463-9	Sequence 9, Appli
28	2459	40.4	4659	1	US-08-232-463-10	Sequence 10, Appl
29	2459	40.4	4818	1	US-08-232-463-11	Sequence 11, Appl
30	2459	40.4	4821	1	US-08-232-463-12	Sequence 12, Appl
31	2459	40.4	4824	1	US-08-232-463-13	Sequence 13, Appl
32	2456.8	40.4	3878	3	US-08-651-472-65	Sequence 65, Appli
33	2456.8	40.4	3878	3	US-08-358-928-65	Sequence 65, Appli
34	2456.8	40.4	4701	3	US-08-651-472-64	Sequence 64, Appli
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37	2456.8	40.4	6474	3	US-08-651-472-66	Sequence 66, Appl
38	2456.8	40.4	6474	3	US-08-358-928-66	Sequence 66, Appl
39	2456.8	40.3	8313	1	US-08-232-463-2	Sequence 2, Appli
40	2456.8	40.4	8775	1	US-08-232-463-3	Sequence 3, Appli
41	2455.2	40.3	9454	1	US-08-232-463-4	Sequence 4, Appli
42	2455.2	40.3	9454	1	US-08-232-463-5	Sequence 5, Appli
43	2449.8	40.2	6601	1	US-08-232-463-14	Sequence 14, Appl
44	2449.8	40.2	7218	1	US-08-232-463-15	Sequence 15, Appl
45	2449.8	40.2	9890	1	US-08-232-463-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-862-431-32
; Sequence 32, Application US/08862431
; Patent No. 6120994
; GENERAL INFORMATION:
; APPLICANT: TAM, SHUI-PANG
; TITLE OF INVENTION: ANTIOXIDANT RESPONSIVE ELEMENT
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,431
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kim, Judith U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 1669.0020000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
US-08-862-431-32

Query Match   50.9%;   Score 3096;   DB 3;   Length 5789;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 3096;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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